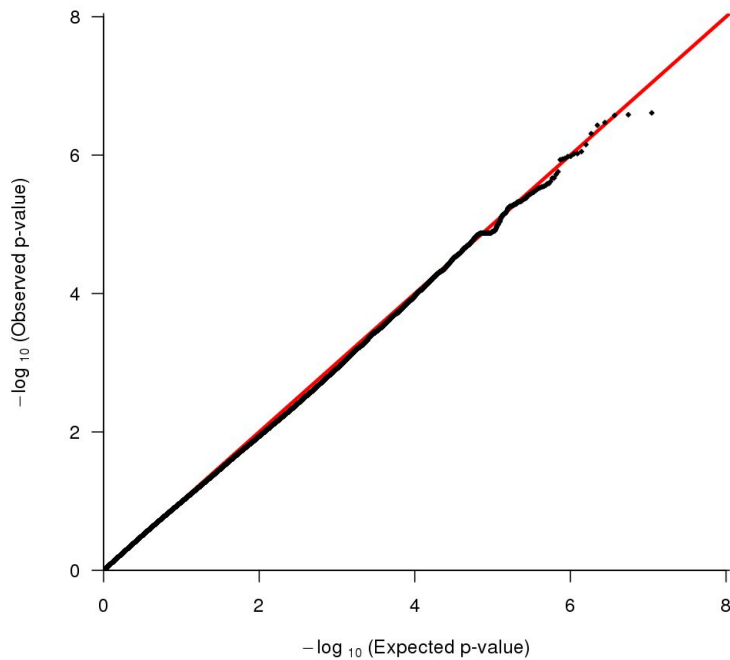


Figure S4. Genome-wide association study of HIV-1 acquisition in 1,142 European Americans from the Urban Health Study. (A) The quantile-quantile plot shows the association results of approximately 8 million tested SNPs and indels. The observed distribution of P values vs. the expected distribution of P values (black dots) is plotted on a logarithmic scale along with the identity line (red), which represents identical observed and expected distributions. The corresponding genomic inflation factor ($\lambda_{gc} = 1.022$) is shown. (B) The $-\log_{10}(P)$ value) are plotted by chromosomal position of SNPs (shown as circles) and indels (shown as triangles). The solid line indicates the threshold for declaring genome-wide statistical significance ($P < 5 \times 10^{-8}$).

(A)



(B)

